

## SEQUENCE LISTING

&lt;110&gt; Curtis, Rory A.J.

<120> 52906, 33408, AND 12189, NOVEL POTASSIUM  
CHANNEL FAMILY MEMBERS AND USES THEREOF

&lt;130&gt; 10448-061001

&lt;150&gt; US 60/209,845

&lt;151&gt; 2000-06-06

&lt;160&gt; 13

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 3525

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (638)...(3178)

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Gln Gln Ser Gln Asp Lys Pro Cys Pro Pro Phe Ala Pro Leu Pro His	
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Val Ser Glu Leu Thr Pro Ser Ser His Ala Ser Ala Leu Arg Gln Gln	
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Tyr Ala Gln Gln Ser Ala Gln Gln Ser Ala Ser Ala Ser Gln Tyr His	
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Gln Cys His Ser Leu Gln Pro Ala Ala Ser Pro Thr Gly Ser Leu Gly	
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Ser Leu Gly Ser Gly Pro Pro Leu Ser His His His His His Pro His	
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Pro Ala His His Gln His His Gln Pro Gln Ala Arg Arg Glu Ser Asn	
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Pro Phe Thr Glu Ile Ala Met Ser Ser Cys Arg Tyr Asn Gly Gly Val	
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Gly Gly Gly Ala Ser Ser Pro Ser Ala Ala Ala Ala Ala Ala Ala	
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Val Ser Ser Ser Ala Pro Glu Ile Val Val Ser Lys Pro Glu His Asn	
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aac tcc aac aac ctg gcg ctc tat gga acc ggc ggc gga ggc agc act	1711
Asn Ser Asn Asn Leu Ala Leu Tyr Gly Thr Gly Gly Gly Gly Ser Thr	
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Thr Lys Ser Ser Lys Lys Lys Asn Gln Asn Ile Gly Tyr Lys Leu Gly	
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His Arg Arg Ala Leu Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala	
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Phe Thr Trp Thr Ala Arg Leu Ala Phe Ser Tyr Ala Pro Ser Thr Thr	
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acc gct gat gtg gat att att tta tct ata cca atg ttc tta aga ctc	2239

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Tyr	Leu	Ile	Ala	Arg	Val	Met	Leu	Leu	His	Ser	Lys	Leu	Phe	Thr	Asp		
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Ala	Cys	Glu	Arg	Tyr	His	Asp	Gln	Gln	Asp	Val	Thr	Ser	Asn	Phe	Leu		
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Asp	Met	Val	Pro	Asn	Thr	Tyr	Cys	Gly	Lys	Gly	Val	Cys	Leu	Leu	Thr		
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Ile Val Thr Leu Glu Thr Lys Leu Glu Thr Leu Ile Gly Ser Ile His			
775	780	785	790
gcc ctc cct ggg ctc ata agc cag acc atc agg cag cag cag aga gat			3055
Ala Leu Pro Gly Leu Ile Ser Gln Thr Ile Arg Gln Gln Gln Arg Asp			
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ttc att gag gct cag atg gag agc tac gac aag cac gtc act tac aat			3103
Phe Ile Glu Ala Gln Met Glu Ser Tyr Asp Lys His Val Thr Tyr Asn			
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Arg Gly Phe Phe Pro Glu Gln Pro Pro Pro Pro Pro Arg Ser Ser His			
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Leu His Cys Gln Gln Gln Gln Gln Ser Gln Asp Lys Pro Cys Pro Pro			
85 90 95			
Phe Ala Pro Leu Pro His Pro His His His Pro His Leu Ala His Gln			
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Ala Ser Ser Gly Ala Pro Ala Ala Gly Ala Gly Asp Asn Leu Ser Leu			
130 135 140			

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 Pro Thr Gly Ser Leu Gly Ser Leu Gly Ser Gly Pro Pro Leu Ser His  
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 His His His His Pro His Pro Ala His His Gln His His Gln Pro Gln  
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 Pro Met Phe Leu Arg Leu Tyr Leu Ile Ala Arg Val Met Leu Leu His  
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 Lys Ile Asn Phe Asn Thr Arg Phe Val Met Lys Thr Leu Met Thr Ile  
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 Ala Ala Trp Thr Val Arg Ala Cys Glu Arg Tyr His Asp Gln Gln Asp

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Gly Val Cys Leu Leu Thr Gly Ile Met Gly Ala Gly Cys Thr Ala Leu		
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His Val His Asn Phe Met Met Asp Thr Gln Leu Thr Lys Arg Val Lys		
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Gln Arg Lys Leu Asn Asp Gln Ala Asn Thr Leu Val Asp Leu Ala Lys		
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755	760	765
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785	790	795
Arg Gln Gln Gln Arg Asp Phe Ile Glu Ala Gln Met Glu Ser Tyr Asp		
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Asn Tyr Glu Ser Asn Cys Phe Glu Val Leu Leu Tyr Lys Lys Asn Arg	90	95	100	
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Thr Pro Val Trp Phe Tyr Met Gln Ile Ala Pro Ile Arg Asn Glu His	105	110	115	
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Glu Lys Val Val Leu Phe Leu Cys Thr Phe Lys Asp Ile Thr Leu Phe	120	125	130	
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970

975

980

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ggagaaagtg tggatgccct ctgctttgtg gtgtcaggat ccttggaagt catccaggat 1800
gatgaggtgg tggctatatt agggaagggt gatgtatttg gagacatctt ctggaaggaa 1860
accacccttg cccatgcatg tgcgaacgtc cgggcactga cgtactgtga cctacacatc 1920
atcaagcggg aagccttgct caaagtccgt gacttttata cagcttttgc aaactccttc 1980
tcaaggaaac tcactcttac ttgcaatctg aggaaacgga tcatctttcg taagatcagt 2040
gatgtgaaga aagaggagga ggagcgccct aggcagaaga atgaggtgac cctcagcatt 2100
cccgtggacc acccagtcag aaagctcttc cagaagttca agcagcagaa ggagctgcgg 2160
aatcagggtc caacacaggg tgaccctgag aggaaccaac tccaggtaga gagccgctcc 2220
ttacagaatg gaacctccat caccggaacc agcgtggtga ctgtgtcaca gattactccc 2280
attcagacgt ctctggccta tgtgaaaacc agtgaatccc ttaagcagaa caaccgtgat 2340
gccatggaac tcaagcccaa cggcgggtgt gacaaaaaat gtctcaaagt caacagccca 2400
ataagaatga agaattgaaa tggaaaaggg tggctgcgac tcaagaataa tatgggagcc 2460
catgaggaga aaaaggaaga ctggaataat gtcactaaag ctgagtcaat ggggctattg 2520
tctgaggacc ccaagagcag tgattcagag aacagtgtga ccaaaaaccc actaaggaaa 2580
acagattctt gtgacagtgg aattacaaaa agtgaccttc gtttggataa ggctggggag 2640
gcccgaagtc cgctagagca cagtcccatc caggctgatg ccaagcacc cttttatccc 2700
atccccgagc aggccttaca gaccacactg caggaagtca aacacgaact caaagaggac 2760
atccagctgc tcagctgcag aatgactgcc ctagaaaagc aggtggcaga aattttaaaa 2820
atactgtcgg aaaaaagcgt accccaggcc tcatctccca aatcccaat gccactccaa 2880
gtaccccccc agataccatg tcaggatatt tttagtgtct caaggcctga atcacctgaa 2940
tctgacaaag atgaaatcca ctttttaa

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&lt;210&gt; 7

&lt;211&gt; 1341

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) ... (1338)

&lt;400&gt; 7

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tgc tgc gag cgg ctg gtg ctc aac gtg gcc ggg ctg cgc ttc gag acg 48
Cys Cys Glu Arg Leu Val Leu Asn Val Ala Gly Leu Arg Phe Glu Thr
1 5 10 15

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```

cgg gcg cgc acg ctg ggc cgc ttc ccg gac act ctg cta ggg gac cca 96
Arg Ala Arg Thr Leu Gly Arg Phe Pro Asp Thr Leu Leu Gly Asp Pro
20 25 30

```

```

gcg cgc cgc ggc cgc ttc tac gac gac gcg cgc cgc gag tat ttc ttc 144
Ala Arg Arg Gly Arg Phe Tyr Asp Asp Ala Arg Arg Glu Tyr Phe Phe
35 40 45

```

```

gac cgg cac cgg ccc agc ttc gac gcc gtg ctc tac tac tac cag tcc 192
Asp Arg His Arg Pro Ser Phe Asp Ala Val Leu Tyr Tyr Tyr Gln Ser
50 55 60

```

```

ggg ggg cgg ctg cgg cgg ccg gcg cac gtg ccg ctc gac gtc ttc ctg 240
Gly Gly Arg Leu Arg Arg Pro Ala His Val Pro Leu Asp Val Phe Leu

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65	70	75	80	
gaa gag gtg gcc ttc tac ggg ctg ggc gcg gcg gcc ctg gca cgc ctg				288
Glu Glu Val Ala Phe Tyr Gly Leu Gly Ala Ala Ala Leu Ala Arg Leu	85	90	95	
cgc gag gac gag ggc tgc ccg gtg ccg ccc gag cgc ccc ctg ccc cgc				336
Arg Glu Asp Glu Gly Cys Pro Val Pro Pro Glu Arg Pro Leu Pro Arg	100	105	110	
cgc gcc ttc gcc cgc cag ctg tgc ctg ctt ttc gag ttt ccc gag agc				384
Arg Ala Phe Ala Arg Gln Leu Cys Leu Leu Phe Glu Phe Pro Glu Ser	115	120	125	
tct cag gcc gcg cgc gtg ctc gcc gta gtc tcc gtg ctg gtc atc ctc				432
Ser Gln Ala Ala Arg Val Leu Ala Val Val Ser Val Leu Val Ile Leu	130	135	140	
gtc tcc atc gtc gtc ttc tgc ctc gag acg ctg cct gac ttc cgc gac				480
Val Ser Ile Val Val Phe Cys Leu Glu Thr Leu Pro Asp Phe Arg Asp	145	150	155	160
gac cgc gac ggc acg ggg ctt gct gct gca gcc gca gcc ggc ccg ttc				528
Asp Arg Asp Gly Thr Gly Leu Ala Ala Ala Ala Ala Ala Gly Pro Phe	165	170	175	
ccc gct ccg ctg aat ggc tcc agc caa atg cct gga aat cca ccc cgc				576
Pro Ala Pro Leu Asn Gly Ser Ser Gln Met Pro Gly Asn Pro Pro Arg	180	185	190	
ctg ccc ttc aat gac ccg ttc ttc gtg gtg gag acg ctg tgt att tgt				624
Leu Pro Phe Asn Asp Pro Phe Phe Val Val Glu Thr Leu Cys Ile Cys	195	200	205	
tgg ttc tcc ttt gag ctg ctg gta cgc ctc ctg gtc tgt cca agc aag				672
Trp Phe Ser Phe Glu Leu Leu Val Arg Leu Leu Val Cys Pro Ser Lys	210	215	220	
gct atc ttc ttc aag aac gtg atg aac ctc atc gat ttt gtg gct atc				720
Ala Ile Phe Phe Lys Asn Val Met Asn Leu Ile Asp Phe Val Ala Ile	225	230	235	240
ctt ccc tac ttt gtg gca ctg ggc acc gag ctg gcc cgg cag cga ggg				768
Leu Pro Tyr Phe Val Ala Leu Gly Thr Glu Leu Ala Arg Gln Arg Gly	245	250	255	
gtg ggc cag cag gcc atg tca ctg gcc atc ctg aga gtc atc cga ttg				816
Val Gly Gln Gln Ala Met Ser Leu Ala Ile Leu Arg Val Ile Arg Leu	260	265	270	
gtg cgt gtc ttc cgc atc ttc aag ctg tcc cgg cac tca aag ggc ctg				864
Val Arg Val Phe Arg Ile Phe Lys Leu Ser Arg His Ser Lys Gly Leu	275	280	285	
caa atc ttg ggc cag acg ctt cgg gcc tcc atg cgt gag ctg ggc ctc				912
Gln Ile Leu Gly Gln Thr Leu Arg Ala Ser Met Arg Glu Leu Gly Leu	290	295	300	

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<400> 8																
Cys	Cys	Glu	Arg	Leu	Val	Leu	Asn	Val	Ala	Gly	Leu	Arg	Phe	Glu	Thr	
1				5					10					15		
Arg	Ala	Arg	Thr	Leu	Gly	Arg	Phe	Pro	Asp	Thr	Leu	Leu	Gly	Asp	Pro	
			20					25					30			
Ala	Arg	Arg	Gly	Arg	Phe	Tyr	Asp	Asp	Ala	Arg	Arg	Glu	Tyr	Phe	Phe	
			35				40					45				
Asp	Arg	His	Arg	Pro	Ser	Phe	Asp	Ala	Val	Leu	Tyr	Tyr	Tyr	Gln	Ser	
	50					55					60					
Gly	Gly	Arg	Leu	Arg	Arg	Pro	Ala	His	Val	Pro	Leu	Asp	Val	Phe	Leu	
65					70					75					80	
Glu	Glu	Val	Ala	Phe	Tyr	Gly	Leu	Gly	Ala	Ala	Ala	Leu	Ala	Arg	Leu	
				85					90					95		

Arg Glu Asp Glu Gly Cys Pro Val Pro Pro Glu Arg Pro Leu Pro Arg  
 100 105 110  
 Arg Ala Phe Ala Arg Gln Leu Cys Leu Leu Phe Glu Phe Pro Glu Ser  
 115 120 125  
 Ser Gln Ala Ala Arg Val Leu Ala Val Val Ser Val Leu Val Ile Leu  
 130 135 140  
 Val Ser Ile Val Val Phe Cys Leu Glu Thr Leu Pro Asp Phe Arg Asp  
 145 150 155 160  
 Asp Arg Asp Gly Thr Gly Leu Ala Ala Ala Ala Gly Pro Phe  
 165 170 175  
 Pro Ala Pro Leu Asn Gly Ser Ser Gln Met Pro Gly Asn Pro Pro Arg  
 180 185 190  
 Leu Pro Phe Asn Asp Pro Phe Phe Val Val Glu Thr Leu Cys Ile Cys  
 195 200 205  
 Trp Phe Ser Phe Glu Leu Leu Val Arg Leu Leu Val Cys Pro Ser Lys  
 210 215 220  
 Ala Ile Phe Phe Lys Asn Val Met Asn Leu Ile Asp Phe Val Ala Ile  
 225 230 235 240  
 Leu Pro Tyr Phe Val Ala Leu Gly Thr Glu Leu Ala Arg Gln Arg Gly  
 245 250 255  
 Val Gly Gln Gln Ala Met Ser Leu Ala Ile Leu Arg Val Ile Arg Leu  
 260 265 270  
 Val Arg Val Phe Arg Ile Phe Lys Leu Ser Arg His Ser Lys Gly Leu  
 275 280 285  
 Gln Ile Leu Gly Gln Thr Leu Arg Ala Ser Met Arg Glu Leu Gly Leu  
 290 295 300  
 Leu Ile Phe Phe Leu Phe Ile Gly Val Val Leu Phe Ser Ser Ala Val  
 305 310 315 320  
 Tyr Phe Ala Glu Val Asp Arg Val Asp Ser His Phe Thr Ser Ile Pro  
 325 330 335  
 Glu Ser Phe Trp Trp Ala Val Val Thr Met Thr Thr Val Gly Tyr Gly  
 340 345 350  
 Asp Met Ala Pro Val Thr Val Gly Gly Lys Ile Val Gly Ser Leu Cys  
 355 360 365  
 Ala Ile Ala Gly Val Leu Thr Ile Ser Leu Pro Val Pro Val Ile Val  
 370 375 380  
 Ser Asn Phe Ser Tyr Phe Tyr His Arg Glu Thr Glu Gly Glu Glu Ala  
 385 390 395 400  
 Gly Met Phe Ser His Val Asp Met Gln Pro Cys Gly Pro Leu Glu Gly  
 405 410 415  
 Lys Ala Asn Gly Gly Leu Val Asp Gly Glu Val Pro Glu Leu Pro Pro  
 420 425 430  
 Pro Leu Trp Ala Pro Pro Gly Lys His Leu Val Thr Glu Val  
 435 440 445

<210> 9

<211> 223

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<400> 9

Ile Leu Phe Ile Leu Asp Leu Leu Phe Val Leu Leu Phe Leu Leu Glu  
 1 5 10 15  
 Ile Val Leu Lys Phe Ile Ala Tyr Gly Leu Lys Ser Thr Ser Asn Ile

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20 25 30  
 Ala Ala Lys Tyr Leu Lys Ser Ile Phe Asn Ile Leu Asp Leu Leu Ala  
 35 40 45  
 Ile Leu Pro Leu Leu Leu Leu Val Leu Phe Leu Ser Gly Thr Glu  
 50 55 60  
 Gln Val Ala Lys Lys Arg Leu Arg Glu Arg Phe Ser Leu Glu Leu Ser  
 65 70 75 80  
 Gln Trp Tyr Tyr Arg Ile Leu Arg Phe Leu Arg Leu Leu Arg Leu Leu  
 85 90 95  
 Arg Leu Leu Arg Leu Leu Arg Leu Leu Arg Arg Leu Glu Thr Leu Phe  
 100 105 110  
 Glu Phe Glu Leu Gly Thr Leu Ala Trp Ser Leu Gln Ser Leu Gly Arg  
 115 120 125  
 Ala Leu Lys Ser Ile Leu Arg Phe Leu Leu Leu Leu Leu Leu Leu  
 130 135 140  
 Ile Gly Phe Ser Val Ile Gly Tyr Leu Leu Phe Lys Gly Tyr Glu Asp  
 145 150 155 160  
 Leu Ser Glu Asn Glu Val Asp Gly Asn Ser Glu Phe Ser Ser Tyr Phe  
 165 170 175  
 Asp Ala Phe Tyr Phe Leu Phe Val Thr Leu Thr Thr Val Gly Phe Gly  
 180 185 190  
 Asp Leu Val Pro Val Trp Leu Gly Ile Ile Phe Phe Val Leu Phe Phe  
 195 200 205  
 Ile Ile Val Gly Leu Leu Leu Leu Asn Leu Leu Ile Ala Val Ile  
 210 215 220

&lt;210&gt; 10

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; consensus sequence

&lt;400&gt; 10

Ala Leu Glu Glu Arg Ser Tyr Pro Ala Gly Glu Val Ile Ile Arg Gln  
 1 5 10 15  
 Gly Asp Pro Gly Asp Ser Phe Tyr Ile Val Leu Ser Gly Glu Val Glu  
 20 25 30  
 Val Tyr Lys Leu Thr Glu Asp Gly Ala Arg Thr Pro Glu Val Ser Gln  
 35 40 45  
 Lys Gln Asp Thr Arg Glu Gln Val Val Ala Thr Leu Gly Pro Gly Asp  
 50 55 60  
 Phe Phe Gly Glu Leu Ala Leu Leu Thr Asn Asp Gly Asn Lys Asn Ala  
 65 70 75 80  
 Val Leu Pro Ser Leu Asp Gln Gly Ala Pro Arg Thr Ala Thr Val Arg  
 85 90 95  
 Ala Leu Thr Asp Ser Glu Leu Leu Arg Leu Asp Arg Glu Asp Phe Arg  
 100 105 110  
 Arg Leu Leu Gln Lys Tyr Pro Glu  
 115 120

&lt;210&gt; 11

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

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&lt;220&gt;

&lt;223&gt; consensus sequence

&lt;400&gt; 11

Glu	Arg	Val	Arg	Leu	Asn	Val	Gly	Gly	Lys	Arg	Phe	Glu	Thr	Ser	Lys
1				5					10					15	
Ser	Thr	Leu	Thr	Arg	Phe	Lys	Pro	Asp	Thr	Leu	Leu	Gly	Arg	Leu	Leu
			20					25					30		
Lys	Thr	Asp	Ser	Asp	Val	His	Glu	Ala	Arg	Leu	Arg	Leu	Cys	Asp	Phe
		35					40					45			
Tyr	Asp	Asp	Glu	Thr	Gly	Glu	Tyr	Phe	Phe	Asp	Arg	Ser	Pro	Lys	His
	50					55				60					
Phe	Glu	Thr	Ile	Leu	Asn	Phe	Tyr	Arg	Thr	Gly	Asp	Gly	Lys	Leu	His
65					70					75					80
Arg	Pro	Glu	Val	Cys	Leu	Asp	Ser	Phe	Leu	Glu	Glu	Leu	Glu	Phe	Tyr
				85					90					95	
Gly	Leu	Asp	Glu	Leu	Ala	Ile	Glu	Ser	Cys	Cys	Glu	Asp	Glu	Tyr	
			100					105					110		

&lt;210&gt; 12

&lt;211&gt; 988

&lt;212&gt; PRT

&lt;213&gt; Rattus norvegicus

&lt;400&gt; 12

Met	Pro	Gly	Gly	Lys	Arg	Gly	Leu	Val	Ala	Pro	Gln	Asn	Thr	Phe	Leu
1				5					10					15	
Glu	Asn	Ile	Val	Arg	Arg	Ser	Ser	Glu	Ser	Ser	Phe	Leu	Leu	Gly	Asn
			20					25					30		
Ala	Gln	Ile	Val	Asp	Trp	Pro	Val	Val	Tyr	Ser	Asn	Asp	Gly	Phe	Cys
		35					40					45			
Lys	Leu	Ser	Gly	Tyr	His	Arg	Ala	Asp	Val	Met	Gln	Lys	Ser	Ser	Thr
	50					55				60					
Cys	Ser	Phe	Met	Tyr	Gly	Glu	Leu	Thr	Asp	Lys	Lys	Thr	Ile	Glu	Lys
65					70					75					80
Val	Arg	Gln	Thr	Phe	Asp	Asn	Tyr	Glu	Ser	Asn	Cys	Phe	Glu	Val	Leu
				85					90					95	
Leu	Tyr	Lys	Lys	Asn	Arg	Thr	Pro	Val	Trp	Phe	Tyr	Met	Gln	Ile	Ala
			100					105					110		
Pro	Ile	Arg	Asn	Glu	His	Glu	Lys	Val	Val	Leu	Phe	Leu	Cys	Thr	Phe
	115					120						125			
Lys	Asp	Ile	Thr	Leu	Phe	Lys	Gln	Pro	Ile	Glu	Asp	Asp	Ser	Thr	Lys
	130					135					140				
Gly	Trp	Thr	Lys	Phe	Ala	Arg	Leu	Thr	Arg	Ala	Leu	Thr	Asn	Ser	Arg
145					150					155					160
Ser	Val	Leu	Gln	Gln	Leu	Thr	Pro	Met	Asn	Lys	Thr	Glu	Thr	Val	His
			165						170					175	
Lys	His	Ser	Arg	Leu	Ala	Glu	Val	Leu	Gln	Leu	Gly	Ser	Asp	Ile	Leu
			180					185					190		
Pro	Gln	Tyr	Lys	Gln	Glu	Ala	Pro	Lys	Thr	Pro	Pro	His	Ile	Ile	Leu
	195						200					205			
His	Tyr	Cys	Ala	Phe	Lys	Thr	Thr	Trp	Asp	Trp	Val	Ile	Leu	Ile	Leu
	210					215					220				
Thr	Phe	Tyr	Thr	Ala	Ile	Met	Val	Pro	Tyr	Asn	Val	Ser	Phe	Lys	Thr
225					230					235					240
Lys	Gln	Asn	Asn	Ile	Ala	Trp	Leu	Val	Leu	Asp	Ser	Val	Val	Asp	Val
				245					250					255	

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Ile Phe Leu Val Asp Ile Val Leu Asn Phe His Thr Thr Phe Val Gly  
 260 265 270  
 Pro Gly Gly Glu Val Ile Ser Asp Pro Lys Leu Ile Arg Met Asn Tyr  
 275 280 285  
 Leu Lys Thr Trp Phe Val Ile Asp Leu Leu Ser Cys Leu Pro Tyr Asp  
 290 295 300  
 Ile Ile Asn Ala Phe Glu Asn Val Asp Glu Gly Ile Ser Ser Leu Phe  
 305 310 315 320  
 Ser Ser Leu Lys Val Val Arg Leu Leu Arg Leu Gly Arg Val Ala Arg  
 325 330 335  
 Lys Leu Asp His Tyr Leu Glu Tyr Gly Ala Ala Val Leu Val Leu Leu  
 340 345 350  
 Val Cys Val Phe Gly Leu Val Ala His Trp Leu Ala Cys Ile Trp Tyr  
 355 360 365  
 Ser Ile Gly Asp Tyr Glu Val Ile Asp Glu Val Thr Asn Thr Ile Gln  
 370 375 380  
 Ile Asp Ser Trp Leu Tyr Gln Leu Ala Leu Ser Ile Arg Thr Pro Tyr  
 385 390 395 400  
 Arg Tyr Asn Thr Ser Ala Gly Ile Trp Glu Gly Gly Pro Ser Lys Asp  
 405 410 415  
 Ser Leu Tyr Val Ser Ser Leu Tyr Phe Thr Met Thr Ser Leu Thr Thr  
 420 425 430  
 Ile Gly Phe Gly Asn Ile Ala Pro Thr Thr Asp Val Glu Lys Met Phe  
 435 440 445  
 Ser Val Ala Met Met Met Val Gly Ser Leu Leu Tyr Ala Thr Ile Phe  
 450 455 460  
 Gly Asn Val Thr Thr Ile Phe Gln Gln Met Tyr Ala Asn Thr Asn Arg  
 465 470 475 480  
 Tyr His Glu Met Leu Asn Asn Val Arg Asp Phe Leu Lys Leu Tyr Gln  
 485 490 495  
 Val Pro Lys Gly Leu Ser Glu Arg Val Met Asp Tyr Ile Val Ser Thr  
 500 505 510  
 Trp Ser Met Ser Lys Gly Ile Asp Thr Glu Lys Val Leu Ser Ile Cys  
 515 520 525  
 Pro Lys Asp Met Arg Ala Asp Ile Cys Val His Leu Asn Arg Lys Val  
 530 535 540  
 Phe Asn Glu His Pro Ala Phe Arg Leu Ala Ser Asp Gly Cys Leu Arg  
 545 550 555 560  
 Ala Leu Ala Val Glu Phe Gln Thr Ile His Cys Ala Pro Gly Asp Leu  
 565 570 575  
 Ile Tyr His Ala Gly Glu Ser Val Asp Ala Leu Cys Phe Val Val Ser  
 580 585 590  
 Gly Ser Leu Glu Val Ile Gln Asp Glu Glu Val Val Ala Ile Leu Gly  
 595 600 605  
 Lys Gly Asp Val Phe Gly Asp Ile Phe Trp Lys Glu Thr Thr Leu Ala  
 610 615 620  
 His Ala Cys Ala Asn Val Arg Ala Leu Thr Tyr Cys Asp Leu His Ile  
 625 630 635 640  
 Ile Lys Arg Glu Ala Leu Leu Lys Val Leu Asp Phe Tyr Thr Ala Phe  
 645 650 655  
 Ala Asn Ser Phe Ser Arg Asn Leu Thr Leu Thr Cys Asn Leu Arg Lys  
 660 665 670  
 Arg Ile Ile Phe Arg Lys Ile Ser Asp Val Lys Lys Glu Glu Glu Glu  
 675 680 685  
 Arg Leu Arg Gln Lys Asn Glu Val Thr Leu Ser Ile Pro Val Asp His  
 690 695 700  
 Pro Val Arg Lys Leu Phe Gln Lys Phe Lys Gln Gln Lys Glu Leu Arg

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705					710					715				720	
Asn	Gln	Gly	Ser	Ala	Gln	Ser	Asp	Pro	Glu	Arg	Ser	Gln	Leu	Gln	Val
				725					730					735	
Glu	Ser	Arg	Pro	Leu	Gln	Asn	Gly	Ala	Ser	Ile	Thr	Gly	Thr	Ser	Val
			740					745					750		
Val	Thr	Val	Ser	Gln	Ile	Thr	Pro	Ile	Gln	Thr	Ser	Leu	Ala	Tyr	Val
		755					760					765			
Lys	Thr	Ser	Glu	Thr	Leu	Lys	Gln	Asn	Asn	Arg	Asp	Ala	Met	Glu	Leu
	770					775					780				
Lys	Pro	Asn	Gly	Gly	Ala	Glu	Pro	Lys	Cys	Leu	Lys	Val	Asn	Ser	Pro
785					790					795					800
Ile	Arg	Met	Lys	Asn	Gly	Asn	Gly	Lys	Gly	Trp	Leu	Arg	Leu	Lys	Asn
			805						810					815	
Asn	Met	Gly	Ala	His	Glu	Glu	Lys	Lys	Glu	Glu	Trp	Asn	Asn	Val	Thr
			820						825					830	
Lys	Ala	Glu	Ser	Met	Gly	Leu	Leu	Ser	Glu	Asp	Pro	Lys	Gly	Ser	Asp
		835					840					845			
Ser	Glu	Asn	Ser	Val	Thr	Lys	Asn	Pro	Leu	Arg	Lys	Thr	Asp	Ser	Cys
	850					855					860				
Asp	Ser	Gly	Ile	Thr	Lys	Ser	Asp	Leu	Arg	Leu	Asp	Lys	Ala	Gly	Glu
865					870					875					880
Ala	Arg	Ser	Pro	Leu	Glu	His	Ser	Pro	Ser	Gln	Ala	Asp	Ala	Lys	His
			885						890					895	
Pro	Phe	Tyr	Pro	Ile	Pro	Glu	Gln	Ala	Leu	Gln	Thr	Thr	Leu	Gln	Glu
			900					905					910		
Val	Lys	His	Glu	Leu	Lys	Glu	Asp	Ile	Gln	Leu	Leu	Ser	Cys	Arg	Met
	915						920					925			
Thr	Ala	Leu	Glu	Lys	Gln	Val	Ala	Glu	Ile	Leu	Lys	Leu	Leu	Ser	Glu
	930					935					940				
Lys	Ser	Val	Pro	Gln	Thr	Ser	Ser	Pro	Lys	Pro	Gln	Ile	Pro	Leu	Gln
945					950					955					960
Val	Pro	Pro	Gln	Ile	Pro	Cys	Gln	Asp	Ile	Phe	Ser	Val	Ser	Arg	Pro
			965					970						975	
Glu	Ser	Pro	Glu	Ser	Asp	Lys	Asp	Glu	Ile	Asn	Phe				
			980					985							

<210> 13  
 <211> 532  
 <212> PRT  
 <213> Mus musculus

<400> 13  
 Met Thr Thr Arg Lys Ala Gln Glu Ile His Gly Lys Ala Pro Gly Gly  
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 Ser Val Ser Thr Gly Val Gly Thr Ala Glu Gly Ala Pro Ser Pro Ala  
 20 25 30  
 Gly Val Thr Pro Pro Pro Pro Pro Arg Pro Gly Arg Thr Phe His Ala  
 35 40 45  
 Ile Phe Thr Arg Arg His Arg Thr Pro Asp Trp Gly Gly Cys Gly Val  
 50 55 60  
 Gly Ala Thr Arg Pro Phe Thr Gly Arg Pro Gly Cys Ala Arg His Gly  
 65 70 75 80  
 Ala Thr Val Pro Ala Ala Leu Arg Cys Cys Glu Arg Leu Val Leu Asn  
 85 90 95  
 Val Ala Gly Leu Arg Phe Glu Thr Arg Ala Arg Thr Leu Gly Arg Phe  
 100 105 110  
 Pro Asp Thr Leu Leu Gly Asp Pro Val Arg Arg Ser Arg Phe Tyr Asp

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	115		120		125										
Gly	Ala	Arg	Ala	Glu	Tyr	Phe	Phe	Asp	Arg	His	Arg	Pro	Ser	Phe	Asp
	130					135					140				
Ala	Val	Leu	Tyr	Tyr	Tyr	Gln	Ser	Gly	Gly	Arg	Leu	Arg	Arg	Pro	Ala
145					150					155					160
His	Val	Pro	Leu	Asp	Val	Phe	Leu	Glu	Glu	Val	Ser	Phe	Tyr	Gly	Leu
				165					170					175	
Gly	Arg	Arg	Leu	Ala	Arg	Leu	Arg	Glu	Asp	Glu	Gly	Cys	Ala	Val	Ala
			180					185					190		
Glu	Arg	Pro	Leu	Pro	Pro	Pro	Phe	Ala	Arg	Gln	Leu	Trp	Leu	Leu	Phe
		195					200					205			
Glu	Phe	Pro	Glu	Ser	Ser	Gln	Ala	Ala	Arg	Val	Leu	Ala	Val	Val	Ser
	210					215					220				
Val	Leu	Val	Ile	Leu	Val	Ser	Ile	Val	Val	Phe	Cys	Leu	Glu	Thr	Leu
225					230					235					240
Pro	Asp	Phe	Arg	Asp	Asp	Arg	Asp	Asp	Pro	Gly	Leu	Ala	Pro	Val	Ala
				245				250						255	
Ala	Ala	Thr	Gly	Ser	Phe	Leu	Ala	Arg	Leu	Asn	Gly	Ser	Ser	Pro	Met
			260					265					270		
Pro	Gly	Ala	Pro	Pro	Arg	Gln	Pro	Phe	Asn	Asp	Pro	Phe	Phe	Val	Val
		275				280						285			
Glu	Thr	Leu	Cys	Ile	Cys	Trp	Phe	Ser	Phe	Glu	Leu	Leu	Val	His	Leu
	290					295					300				
Val	Ala	Cys	Pro	Ser	Lys	Ala	Val	Phe	Phe	Lys	Asn	Val	Met	Asn	Leu
305					310					315					320
Ile	Asp	Phe	Val	Ala	Ile	Leu	Pro	Tyr	Phe	Val	Ala	Leu	Gly	Thr	Glu
				325					330					335	
Leu	Ala	Arg	Gln	Arg	Gly	Val	Gly	Gln	Pro	Ala	Met	Ser	Leu	Ala	Ile
			340					345					350		
Leu	Arg	Val	Ile	Arg	Leu	Val	Arg	Val	Phe	Arg	Ile	Phe	Lys	Leu	Ser
		355					360					365			
Arg	His	Ser	Lys	Gly	Leu	Gln	Ile	Leu	Gly	Gln	Thr	Leu	Arg	Ala	Ser
	370					375					380				
Met	Arg	Glu	Leu	Gly	Leu	Leu	Ile	Phe	Phe	Leu	Phe	Ile	Gly	Val	Val
385					390					395					400
Leu	Phe	Ser	Ser	Ala	Val	Tyr	Phe	Ala	Glu	Val	Asp	Arg	Val	Asp	Thr
				405					410					415	
His	Phe	Thr	Ser	Ile	Pro	Glu	Ser	Phe	Trp	Trp	Ala	Val	Val	Thr	Met
			420					425					430		
Thr	Thr	Val	Gly	Tyr	Gly	Asp	Met	Ala	Pro	Val	Thr	Val	Gly	Gly	Lys
		435					440					445			
Ile	Val	Gly	Ser	Leu	Cys	Ala	Ile	Ala	Gly	Val	Leu	Thr	Ile	Ser	Leu
	450					455					460				
Pro	Val	Pro	Val	Ile	Val	Ser	Asn	Phe	Ser	Tyr	Phe	Tyr	His	Arg	Glu
465					470					475					480
Thr	Glu	Gly	Glu	Glu	Ala	Gly	Met	Tyr	Ser	His	Val	Asp	Thr	Gln	Pro
				485				490						495	
Cys	Gly	Thr	Leu	Glu	Gly	Lys	Ala	Asn	Gly	Gly	Leu	Val	Asp	Ser	Glu
			500					505					510		
Val	Pro	Glu	Leu	Leu	Pro	Pro	Leu	Trp	Pro	Pro	Ala	Gly	Lys	His	Met
		515					520					525			
Val	Thr	Glu	Val												
	530														

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